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Project Report: Laboratory Studies of the Origins of an RNA World

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Project Progress

We are continuing our investigation into the smallest number of RNA molecules that can yield active RNA structures, now using experimental rather than theoretical approaches. This work is not ready for a detailed report yet. However, other related work has yielded interesting results, now being prepared for publication. These related experiments determine the number of consecutive randomized nucleotides required to isolate the simplest isoleucine binding RNA by selection. Interestingly, this work shows that unexpectedly short RNA molecules are best, the binding activity being most easily isolated with 26 consecutive random nucleotides. This is much shorter than expected, and in particular, the fact that added nucleotides (to make longer starting sequences) is not helpful (but instead somewhat inhibitory) is particularly hard to explain. What seems to be implied is that there is an unanticipated potent difficulty inhibiting the search for RNA active sites in longer starting sequences.

Highlights

 Short RNA sequences, like those that may have been available to an RNA world with rudimentary RNA synthetic ability, are surprisingly the most competent sequences available for finding RNA binding sites and ribozymes.

Roadmap Objectives

• Objective No. 3.2: Origins and evolution of functional biomolecules